

```

1 GCGTCGCGG CGCGGGGAGA AAGAAGCCGC GCCCAGCCCG GCGTCCCGAG
51 CAGCGCAGGG GAGGATCCCC GCGCAGTGAC CCGGGAGCCA CCACAGACTC
101 TGGGAGGCTC GGCGGCTGGA GCAGCAGGCA GCTCCCCGCA GCTCCCCGCG
151 CTTCCAGGCA GCTCTCTGAG CCGTGCCAGA GGCCCGGCCC GCCATTCCCA
201 GCCCCGAGCC ATGATGAAGA CTTTGTCCAG CGGGAAGTGC ACGCTCAGTG
251 TGCCCCGCAA AAACCTCATAC CGCATGGTGG TGCTGGGTGC CTCTCGGGTG
301 GGCAAGAGCT CCATCGTGTC TCGCTTCCTC AATGGCCGCT TTGAGGACCA
351 GTACACACCC ACCATCGAGG ACTTCCACCG TAAGGTATAC AACATCCGCG
401 GCGACATGTA CCAGCTCGAC ATCCTGGATA CCTCTGGCAA CCACCCCTTC
451 CCCGCCATGC GCAGGCTGTC CATCCTCACA GGGGATGTCT TCATCCTGGT
501 GTTCAGCCTG GATAACCGGG AGTCCTTCGA TGAGGTCAAG CGCCTTCAGA
551 AGCAGATCCT GGAGGTCAAG TCCTGCCTGA AGAACAAGAC CAAGGAGGCG
601 GCGGAGCTGC CCATGGTCAT CTGTGGCAAC AAGAACGACC ACGGCGAGCT
651 GTGCCGCCAG GTGCCACCA CCGAGGCCGA GCTGCTGGTG TCGGGCGACG
701 AGAACTCCGC CTACTTCGAG GTGTCGGCCA AGAAGAACAC CAACGTGGAC
751 GAGATGTTCT ACGTGCTCTT CAGCATGGCC AAGCTGCCAC ACGAGATGAG
801 CCCCGCCTTG CATCGCAAGA TCTCCGTGCA GTACGGTGAC GCCTTCCACC
851 CCAGGCCCTT CTGCATGCGC CGCGTCAAGG AGATGGACGC CTATGGCATG
901 GTCTCGCCTT TCGCCCGCCG CCCCAGCGTC AACAGTGACC TCAAGTACAT
951 CAAGGCCAAG GTCCTTCGGG AAGGCCAGGC CCGTGAGAGG GACAAGTGCA
1001 CCATCCAGTG AGCGAGGGAT GCTGGGGCGG GGCTTGGCCA GTGCCTTCAG
1051 GGAGGTGGCC CCAGATGCCC ACTGTGCGCA TCTCCCACC GAGGCCCGCG
1101 CAGCAGTCTT GTTCACAGAC CTTAGGCACC AGACTGGAGG CCCCAGGGCG
1151 CTGGCCTCCG CACATTCGTC TGCCTTCTCA CAGCTTTCCT GAGTCCGCTT
1201 GTCCACAGCT CTTGGTGGT TTCATCTCCT CTGTGGGAGG ACACATCTCT
1251 GCAGCCTCAA GAGTTAGGCA GAGACTCAAG TTACACCTTC CTCTCCTGGG
1301 GTTGAAGAA ATGTTGATGC CAGAGGGGTG AGGATTGCTG CGTCATATGG
1351 AGCCTCCTGG GACAAGCCTC AGGATGAAAA GGACACAGAA GGCCAGATGA
1401 GAAAGGTCTC CTCTCTCCTG GCATAACACC CAGCTTGGTT TGGGTGGCAG
1451 CTGGGAGAAC TTCTCTCCCA GCCCTGCAAC TCTTACGCTC TGGTTCAGCT
1501 GCCTCTGCAC CCCCTCCCAC CCCCAGCACA CACACAAGTT GGCCCCCAGC
1551 TGGCCTGAC ATTGAGCCAG TGGACTCTGT GTCTGAAGGG GGCGTGCCCA
1601 CACCTCCTAG ACCACGCCCA CCACTTAGAC CACGCCACC TCCTGACCGC
1651 GTTCTCAGC CTCTCTCCT AGGTCCCTCC GCCCGACAGT TGTGCTTTGT
1701 TGTGGTTGCA GCTGTTTTCG TGTCATGTAT AGTAGTAGAA ATGGAATCA
1751 TTGTACTGTA AAAGCCTAGT GACTCCCTCC TTGGCCAGGC CCTCACCAG
1801 TTCAGATCCA CGGCCTCCAC CCGGGACGCC TTCCTCCTCT GCTCCCAAAC
1851 AGGGTTTCCG TGGCCTGTTT GCAGCTAGAC ATTGACCTCC GCCATTGAGC
1901 TCCACGGTTT ACAGACAATT GCACAAGCGT GGGGTGGGCA GGCCAGGACT
1951 GCTTTTTTTT AATGCTCCCA TTTCACAGAG GATACCACCG AGACTCGGAG
2001 GGGACACGAT GAGCACCAGG CCCCACCTTT GTCCCCTAGC AAATTCAGGG
2051 TACAGCTCCA CCTAGAACCA GGCTGCCCTC TACTGTGCTC GTTCCTCAAG
2101 CATTATTATA GCACCTACTG GGTGCTGGGT TCACTGTGTC CTAGGAAACC
2151 AAGAGGGTCC CCAGTCCTGG CCTCTGCCCG CCCCTGCTGC CCCACCACCT
2201 TCTGCACACA CAGCGGTGGG GAGGCGGGGA GGAGCAGCTG GGACCCAGAA
2251 CTGAGCCTGG GAGGGATCCG ACAGAAAAGC TCAGGGCGGG TCTTCTCCTT
2301 GTGCCCGGGA TTGGGCTATG CTGGGTACCA CCATGTACTC AGGCATGGTG
2351 GGTTTTGAAC CCATAAACCA AAGGCCCTTG TCATCAGCTC TTAACAAGTA
2401 TATTTTGTAT TTTAATCTCT CTAAACATAT TGAAGTTTAA GGGCCCTAAG
2451 GAACCTTAGT GATCTTCTAT TGGGTCTTTC TGAGGTTTCA AGAGGGTAAG
2501 TAACTTCCTC CAGGTACAC AGCAAGTCTG TGGGTGGCAG AAGCAAGCTA
2551 GCGCTGGGCA TTCAGTACAT ACCACGATGT GCTCCCTCTC TTGATGCTTG
2601 GCCCCTGGGG CTTTCAGGGC TTTGGGACAT CTTGTCTCTA ACCCTCTCCC
2651 TAGATCAGTC TGTGAGGGTC CCTGTAGATA TTGTGTACAC CATGCCCATG
2701 TATATACAAG TACACACAGA TGTACACACA GATGTACACA TGCTCCAGCC
2751 CCAGCTCTGC ATACCTGCAC CTGCACCCCA GCCTTGGCCC CTGCTGCGT
2801 CTGTGCTCAA AGCAGCAGCT CCAACCCTGC CTCTGTCCCC TTCCCCACCC
2851 ACTGCTGAG CTTCTGAGC AGACCAGGTA CTTGGCTGTC ACCGGTGTGT
2901 GGCCCGCTCT CACCCAGGCA CAGCCCCGCC ACCATGGATC TCCGTGTACA
2951 CTATCAATAA AAGTGGGTTT GTTACAAAAA AAAAAAAAAA AAAAAAAAAA
3001 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA
3051 AAAAAAAAAA AAAAAAAAAA AAAAAAAAAA AA

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FIGURE 1, page 1 of 3

FEATURES:

5'UTR: 1-210
Start Codon: 211
Stop Codon: 1009
3'UTR: 1012

5' UTR ANALYSIS:

Query=cDNA clone
Sbjct: genomic sequence

5' UTR Exon 1, non-coding

Score = 58.0 bits (29), Expect = 2e-10
Identities = 29/29 (100%)
Strand = Plus / Plus

Query: 1 ggcgtcgccgcgcggggagaaaagaagccg 29
|||||
Sbjct: 1535 ggcgtcgccgcgcggggagaaaagaagccg 1563

5' UTR Exon 2, non-coding

Score = 349 bits (176), Expect = 3e-98
Identities = 176/176 (100%)
Strand = Plus / Plus

Query: 26 gccgcgcccagcccggcggtcccgagcagcgcaggggaggatccccgcgcagtgacccggg 85
|||||
Sbjct: 2001 gccgcgcccagcccggcggtcccgagcagcgcaggggaggatccccgcgcagtgacccggg 2060

Query: 86 agccaccacagactctgggaggctcggcggctggagcagcaggcagctccccgcagctcc 145
|||||
Sbjct: 2061 agccaccacagactctgggaggctcggcggctggagcagcaggcagctccccgcagctcc 2120

Query: 146 cggcgcttccaggcagctctctgagccgtgccagaggcccgcccgccattcccag 201
|||||
Sbjct: 2121 cggcgcttccaggcagctctctgagccgtgccagaggcccgcccgccattcccag 2176

Score = 563 bits (284), Expect = e-162
Identities = 284/284 (100%)
Strand = Plus / Plus

5' UTR Exon 3, Protein coding region begins at nucleotide 211

Query: 199 cagccccgagccatgatgaagactttgtccagcggaactgcacgctcagtggtgcccgcc 258
|||||
Sbjct: 7474 cagccccgagccatgatgaagactttgtccagcggaactgcacgctcagtggtgcccgcc 7533

Homologous proteins:**Top BLAST Hits**

	Score	E
CRA 18000005194969 /altid=gi 10047088 /def=ref NP_055125.1 sim...	538	e-152
CRA 18000005238449 /altid=gi 5059122 /def=gb AAD38928.1 AF13440...	512	e-144
CRA 332000009620725 /altid=gi 8118457 /def=gb AAF72997.1 AF2620...	342	2e-93
CRA 18000005232775 /altid=gi 7706359 /def=ref NP_057168.1 ras...	342	2e-93
CRA 87000000006130 /altid=gi 7230768 /def=gb AAF43090.1 AF23915...	342	3e-93
CRA 18000005090459 /altid=gi 6677673 /def=ref NP_033052.1 RAS,...	341	6e-93
CRA 89000000197633 /altid=gi 7295299 /def=gb AAF50620.1 (AE003...	228	8e-59
CRA 105000014645240 /altid=gi 10503969 /def=gb AAG17979.1 AF177...	214	1e-54

BLAST dbEST hits:

gi 9345313 /dataset=dbest /taxon=960...	880	0.0
gi 9335874 /dataset=dbest /taxon=960...	846	0.0
gi 10143211 /dataset=dbest /taxon=96...	821	0.0
gi 9335309 /dataset=dbest /taxon=960...	813	0.0
gi 9150610 /dataset=dbest /taxon=9606...	662	0.0
gi 10144589 /dataset=dbest /taxon=96...	617	e-174
gi 9333908 /dataset=dbest /taxon=960...	599	e-169

EXPRESSION INFORMATION FOR MODULATORY USE:

library source:

Expression information from BLAST dbEST hits:

gi 9345313	Placenta choriocarcinoma
gi 9335874	Uterus endometrium adenocarcinoma
gi 10143211	Skin melanotic melanoma
gi 9335309	Uterus endometrium adenocarcinoma
gi 9150610	Skin melanotic melanoma
gi 10144589	Skin melanotic melanoma
gi 9333908	Uterus endometrium adenocarcinoma

Expression information from PCR-based tissue screening panels:

Human fetal whole brain

408020-0903260

1 MMKTLSSGNC TLSVPAKNSY RMVVLGASRV GKSSIVSRFL NGRFEDQYTP
 51 TIEDFHRKVY NIRGDMYQLD ILDTSGNHPF PAMRRLSILT GDVFILVFSL
 101 DNRESFDEVK RLQKQILEVK SCLKNKTKEA AELPMVICGN KNDHGELCRQ
 151 VPTTEAELLV SGDENSAYFE VSAKKNTNVD EMFYVLFSMA KLPHEMSPAL
 201 HRKISVQYGD AFHPRPFCMR RVKEMDAYGM VSPFARRPSV NSDLKYIAK
 251 VLREGQARER DKCTIQ

FEATURES:

Functional domains and key regions:

[1] PDOC00001 PS00001 ASN_GLYCOSYLATION
 N-glycosylation site

Number of matches: 2

1 9-12 NCTL
 2 125-128 NKTK

[2] PDOC00004 PS00004 CAMP_PHOSPHO_SITE
 CAMP- and cGMP-dependent protein kinase phosphorylation site

Number of matches: 4

1 84-87 RRLS
 2 174-177 KKNT
 3 202-205 RKIS
 4 236-239 RRPS

[3] PDOC00005 PS00005 PKC_PHOSPHO_SITE
 Protein kinase C phosphorylation site

Number of matches: 2

1 19-21 SYR
 2 172-174 SAK

[4] PDOC00006 PS00006 CK2_PHOSPHO_SITE
 Casein kinase II phosphorylation site

Number of matches: 5

1 51-54 TIED
 2 105-108 SFDE
 3 154-157 TEAE
 4 161-164 SGDE
 5 177-180 TNVD

[5] PDOC00007 PS00007 TYR_PHOSPHO_SITE
 Tyrosine kinase phosphorylation site

220-228 RRVKEMDAY

[6] PDOC00266 PS00294 PRENYLATION
 Prenyl group binding site (CAAX box)

263-266 CTIQ

[7] PDOC00016 PS00016 RGD
 Cell attachment sequence

63-65 RGD

[8] PDOC00017 PS00017 ATP_GTP_A
 ATP/GTP-binding site motif A (P-loop)

26-33 GASRVGKS

0977863-00001

BLAST Alignment to Top Hit:

>CRA|18000005194969 /altid=gi|10047088 /def=ref|NP_055125.1| similar
to mouse Ras, dexamethasone-induced 1; tumor endothelial
marker 2 [Homo sapiens] /org=Homo sapiens /taxon=9606
/dataset=nraa /length=278
Length = 278

Score = 538 bits (1372), Expect = e-152
Identities = 265/266 (99%), Positives = 265/266 (99%)

Query: 1 MMKTLSSGNCTLSVPAKNSYRMVVLGASRVGKSSIVSRFLNGRFEDQYTPTIEDFHRKVY 60
MMKTLSSGNCTLSVPAKNSYRMVVLGASRVGKSSIVSRFLNGRFEDQYTPTIEDFHRKVY
Sbjct: 13 MMKTLSSGNCTLSVPAKNSYRMVVLGASRVGKSSIVSRFLNGRFEDQYTPTIEDFHRKVY 72

Query: 61 NIRGDMYQLDILDTSGNHPPFAMRRLSILTGDVFILVFSLDNRESFDEVKRLQKQILEVK 120
NIRGDMYQLDILDTSGNHPPFAMRRLSILTGDVFILVFSLDNRESFDEVKRLQKQILEVK
Sbjct: 73 NIRGDMYQLDILDTSGNHPPFAMRRLSILTGDVFILVFSLDNRESFDEVKRLQKQILEVK 132

Query: 121 SCLKNKTKEAAELPMVICGNKNDHGELCRQVPTTEAELLVSGDENSAYFEVSACKNTNVD 180
SCLKNKTKEAAELPMVICGNKNDHGELCRQVPTTEAELLVSGDEN AYFEVSACKNTNVD
Sbjct: 133 SCLKNKTKEAAELPMVICGNKNDHGELCRQVPTTEAELLVSGDENCAYFEVSACKNTNVD 192

Query: 181 EMFYVLFMAKLPHEMSPALHRKISVQYGDAFHPRPFCMRRVKEMDAYGMVSPFARRPSV 240
EMFYVLFMAKLPHEMSPALHRKISVQYGDAFHPRPFCMRRVKEMDAYGMVSPFARRPSV
Sbjct: 193 EMFYVLFMAKLPHEMSPALHRKISVQYGDAFHPRPFCMRRVKEMDAYGMVSPFARRPSV 252

Query: 241 NSDLKYIKAKVLREGQARERDKCTIQ 266
NSDLKYIKAKVLREGQARERDKCTIQ
Sbjct: 253 NSDLKYIKAKVLREGQARERDKCTIQ 278

Complete Amino Acid Sequence of gi|10047088 /def=ref|NP_055125.1| similar
to mouse Ras, dexamethasone-induced 1; tumor endothelial
marker 2 [Homo sapiens] /org=Homo sapiens /taxon=9606
/dataset=nraa /length=278
Length = 278

NOTE: UNDERLINED RESIDUES NOT PRESENT IN THE PROTEIN OF THE PRESENT INVENTION

1 mpaslallgp rammktlssg nctlsvpakn syrmvvlgas rvgkssivsr flngrfedqy
61 tptiedfhrk vynirgdmq ldildtsgnh pfpamrrlsi ltgdvfilvf sldnresfde
121 vkrlqkqile vksclnkntk eaaelpmvic gnkndhgelt rqvptteael lvsgdencay
181 fevsackntn vdemfyvlfs maklphemsp alhrkisvqy gdafhprpfc mrrvkemday
241 gmvspfarrp svnsdlkyik akvlregqar erdkctiq

>CRA|18000005238449 /altid=gi|5059122 /def=gb|AAD38928.1|AF134409_1
(AF134409) Rhes protein [Rattus norvegicus] /org=Rattus
norvegicus /taxon=10116 /dataset=nraa /length=266
Length = 266

Score = 512 bits (1304), Expect = e-144
Identities = 252/266 (94%), Positives = 256/266 (95%)

Query: 1 MMKTLSSGNCTLSVPAKNSYRMVVLGASRVGKSSIVSRFLNGRFEDQYTPTIEDFHRKVY 60
MMKTLSSGNCTLSVPAKNSYRMVVLGASRVGKSSIVSRFLNGRFEDQYTPTIEDFHRKVY
Sbjct: 1 MMKTLSSGNCTLSVPAKNSYRMVVLGASRVGKSSIVSRFLNGRFEDQYTPTIEDFHRKVY 60

Query: 61 NIRGDMYQLDILDTSGNHPPFAMRRLSILTGDVFILVFSLDNRESFDEVKRLQKQILEVK 120
NI GDMYQLDILDTSGNHPPFAMRRLSILTGDVFILVFSLD+RESFDEVKRLQKQILEVK
Sbjct: 61 NIHGDMYQLDILDTSGNHPPFAMRRLSILTGDVFILVFSLDRESFDEVKRLQKQILEVK 120

Query: 121 SCLKNKTKEAAELPMVICGNKNDHGELCRQVPTTEAELLVSGDENSAYFEVSACKNTNVD 180
SCLKNKTKEAAELPMVICGNKNDH ELCRQVP EAELLVSGDEN AYFEVSACKNTNV+
Sbjct: 121 SCLKNKTKEAAELPMVICGNKNDHSELCRQVPAMEAELLVSGDENCAYFEVSACKNTNVN 180

Query: 181 EMFYVLFSMAKLPHEMSPALHRKISVQYGDAFHPRPFCMRRVKEMDAYGMVSPFARRPSV 240
 EMFYVLFSMAKLPHEMSPALH KISVQYGDAFHPRPFCMRR K AYGMVSPFARRPSV
 Sbjct: 181 EMFYVLFSMAKLPHEMSPALHHKISVQYGDAFHPRPFCMRRTKVAGAYGMVSPFARRPSV 240

Query: 241 NSDLKYIKAKVLREGQARERDKCTIQ 266
 NSDLKYIKAKVLREGQARERDKC+IQ
 Sbjct: 241 NSDLKYIKAKVLREGQARERDKCSIQ 266

Hmmer search results (Pfam):

Model	Description	Score	E-value	N
PF00071	Ras family	126.2	2.8e-36	1
CE00060	CE00060 rab_ras_like	20.7	0.00013	2

Parsed for domains:

Model	Domain	seq-f	seq-t	hmm-f	hmm-t	score	E-value
CE00060	1/2	22	52 ..	26	56 ..	16.9	0.0014
CE00060	2/2	162	183 ..	159	181 ..	3.3	7.5
PF00071	1/1	21	186 ..	1	169 [.	126.2	2.8e-36

09778963-030304

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1 CTCTCTGACT CTTTGCCTCC TCTCTGACTC CCTGCCTCCT CTCTCTGTCT
51 CCCTGCCTCC TCTGTCTGAC TCCCTGCCTC CCCTCTCTGT CTCCTGCCT
101 CCTCTCTCTG ACTCTCTGCC TCCTCTCTCT GACTCCCTGC CTCCTCTCTC
151 TGATTCCCTG CCTCTTTGAC CCTCTGCCTC CTCTCTTTGA CTCCCTGCCT
201 CCTCTCTCCG ATCTCTCTGCG TCTTTGACTC CCTGCCTCCT CTCTCTGACT
251 CCCTGAAGCT CATTCACTCA TTGCTATCAA CTCGTCTGTA CCAAGCTCTA
301 GGCTGGAGGC TGGGCAGGGC AATGATGGAG ACAAATACTG TCCCTGGGAG
351 CTTCTGGCCC CTTTCCCATC CTGTTTAGAC AGAAGTGACC GCCAGCAGAG
401 TCAAGCTGTC TGCAGAAGGA CTTGGGGAGG GGGCTGTCAT GGGGTAGGGC
451 TTCTTTCCCC CCATCTCTGC TGAAGGCCCA GGCTGGCTGA GACAGCCCCG
501 GCAGAGACTG AGAAGGGCTC CCTGCTGTGG TCTGGCAGCC CCCTCTCCAC
551 CCTCTCTCTT CTCTCTCTCT GCCTCCACA CGTATGCCCT GGGCACCTCA
601 TCAGGGCTGC CCTAGGGGAG GGCCCTCCTT GGCACAGCCC CTGGGCCAGT
651 CAGGTGGTTG AGGCTGAGGA GAGAAGGTCC CAGAGTGGGG CTTCAGGCAA
701 ACCCAAAGAC AGAGCCCTTT GCCATTGAT GAATGCACAG ACCCTTTATT
751 GAGCCCTTGC TCTGTTCATG GCATGGCAGT TTTGTGGGAT AAATTCAAAG
801 ACAGCTTTAG GTGGGAGCTG GGTGGGGGAT GTGGGGGTCT TAGGCTTGAA
851 CTACTACCCA GCCTCCTTTG TTAACCAAGT AGCTAGTCAC GTAGCCTTCT
901 GAGCTCGGGG CAGACCACCT GGGATCAAAC CTCTCCTCTG CTGGTTACTG
951 GCTGTGCAAC TGTAAGCAAG TAATTTAACC TCTCTGTGCC TCAGTTTCCT
1001 CATCTGTAAT TTGGAGAATA ACACCACCTG CTTTCTGGGG TTATGAAGGG
1051 AGAAATAGGT TAACATGTGT GCAGCACTTA GAACACTCTG GCATATTTTA
1101 GCTGCAAAAT GAATGCCAGC TATGATTATT TCTATACTTA GTGCGGGGCT
1151 TGGCACACTG CATGGGCTCA AGTGGCAGCA GTTGTCTGCC TTGTGGCTCC
1201 AGGCTTGGGG TCCGCGGTGT GCTGAGCTGG CTTATTGTGC ACGTCCCTTT
1251 GTGATTCATT CATCGAAGTC ACATTAGTAG CTTAGAAGTG ACCGTAGTGG
1301 GAGCATTTAC GCCATGGAAT TTGGCAATAG GGCTTTTAAC AAAGGTATTT
1351 TTGAGAGCCG GTTTCCTGCA CAGAGGCTGG TAGTTGGGCA GGGTGAGCAG
1401 ATCCAGATGT GTGCCAGGGA CTCGCACGCA GGCAATCTCT CCACCTCCAG
1451 TGGCCATCTC AGACCTTAGC TTCATGATAG CCAGGAAGCG ATGGTGTGG
1501 AAAGCGCCTT GGGTCAATGG GCGAGGCACT CAAGGAAACC GACTTGGGGC
1551 ATCCTTGGGT GGGGACCGAG TTTGGGCACA TACAGCCCTT TGTGTGAATT
1601 TAAAAACAGT GCCTTTTCCT CTACACAAGA TGCCCTTTCT TCTGGGATAC
1651 AGCCCCCACC TCTGGGATGC AGCCCCCACT TGCCCCCA GGCATGCGCC
1701 TTGTGAGTA TCCAACCTGC ACAACCTGTG GCAGCCTGTG GAAGACCGAG
1751 GGGATTGATA TTTCAGCAGG CCTGTGCCCA TTTGCAGTTC AGGGGCTGGA
1801 AAGCTCTCCT CTGGAGAGGG GAGGGATTCC TGCAAGGGTG AGGAGATCAG
1851 AGAGGCCTT AGAGAGCAGG TGGCACTTGA GCCAGACCTT GAAACATAAG
1901 GGGAAAGAGG TGTTCTGCAG AGGGGTGGCA TGAGCAAAGG AGTGAGGCT
1951 GATCTCAGCA GAGCTCAAAC TGACGAGGGT GACTGGGGTC AGGGGTCTCTG
2001 GGGCGGGGAT TCTGGTGGGC GCTAAGGTAG GAAAGGAGGG AGGGCTGGGC
2051 TGTGAAGAGC CTTTGGGGTG AGCCTGGTGG AGCCTGCGGG TTTGCTTATA
2101 CAAGAGCTTG GATCCATGTC GGCTCTTTTC ATGAGGTCAA GAGGCTCCCA
2151 TAGAAAGCTC TGAGTTTGGC CCAGAACCAT AACCCTTGA GATGGGAGGG
2201 AAGCTTGAGC CAGCATGGG TCGTTCCCA TTCCACATCC TCTACTCCGG
2251 GCCTCTGGGT CTCCTGGAGG CAAGTAAACA CCTAGGGCCT GGGAGGCAAA
2301 AATATCCGGG CAGGTCATGG AGCGGAGGGA GCGCGCAGA TGCAGAGCAC
2351 AGGTCTAAAG GTGGGTCCCT CTGAGGTGGC TGCAGGAGCA ACCCAGGCA
2401 TTGGGCTTGG AGCATGCGGT GTGGACATAG CTTTCCCTTC TTCCAGGAG
2451 GGCTGAATGG CCACAGAACC ACCCCTGCC CCAGGCTTAA GAAATGCATG
2501 CTAGTGCCTT CCCATGTCT TATCCTAGAA TCACAGGCTC CGGGAAAGCC
2551 AGATGGATGA ACCAGGAAA GAACGGATTC TCACCATAGA TACCATTTTT
2601 GAGATTTTAC CATGTGCTGA GCCCTTTGCA ACAACTCTAT GAATTGGGCT
2651 CATTTTGCAG ATGAGAAAAG TGACTTCTAG AGAGGTTAAG CTACTAGCCC
2701 AAGATCAGTA GCTAGAGGCA AGGCAAGGAT TCAAATCCCA GGAGTCCGGT
2751 GCTTGCAATA ATGAAAGGAT GAATGAACGG ATATTGAGTG AGTGAGTGGA
2801 TGAAGGAAG AGTAAAGGAG AGGGCATGAA TGAATGAGAG GGTAGAACTC
2851 CAAGACCCCT TAGAACCTCG TCTGATGTTT CCATTTTACA GACAGAAAAC
2901 TGAGTCCTAG ACAGAGGCCT AGAGGAGGCC AAGAGGTGGT GGGGCCAGGT
2951 CGGGGGGGCC CTGATGCCTG CTTCTCTCGC TTTGTTGCAG CCCCAGCCA
3001 TGATGAAGAC TTTGTCCAGC GGGAACTGCA CGCTCAGTGT GCGCGCAAA
3051 AACTCATACC GCATGGTGGT GCTGGGTGCC TCTCGGTGG GCAAGAGCTC
3101 CATCGTGTCT CGCTTCCTCA ATGGCCGCTT TGAGGACCAG TACACACCA

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FIGURE 3, page 1 of 6

3151	CCATCGAGGA	CTTCCACCGT	AAGGTATACA	ACATCCGCGG	CGACATGTAC
3201	CAGCTCGACA	TCCTGGATAC	CTCTGGCAAC	CACCCCTTCC	CCGCCATGCG
3251	CAGGCTGTCC	ATCCTCACAG	GTGAGGCCCA	CTGGTGCCCTG	GGCTGGGGCG
3301	GCAGGGCCAG	GGCATGGGTG	CGGAGTGTGC	TGGGCACTTG	GCAGTTTGCA
3351	TAGACTTGCA	TAGCCATCGT	CTGAGACAGG	CGTCATCCCT	GCACAATGAG
3401	GCTCAGAGAG	GTTTTGCCAT	GTGCTGGAAG	TAGTGATGAA	GTGCGGGGCC
3451	CCGATTCCAT	TCTGTTAGAC	TCCAGATCGA	TTACTCATGG	CTGTCGGGGC
3501	CGCCTTCCAG	ATCAGGAGCT	GATACCAGCA	TGCCCCAGGG	ATATTCTTTT
3551	CTAGGGAACA	GAATGATGCC	CTGGCTGCTG	CTTTCTTTCT	CCGGAAGATG
3601	ACCCACCAGA	GCTCCAGGGC	CCAAGGTCAG	TCCACGGGGC	TCAGGTCTCC
3651	CACACCCAG	GCCTTTTGCA	CCTCCTAGAG	AGGTAAGGGC	AGGACCCAGG
3701	CAGTGTGAC	CAAGGGGAAG	GGGGCTTGGT	CATGGTCATA	GTGATGGTGA
3751	TGGCACTAGC	TGACACTTAT	CAGAAGCTAT	GGGCTGGCC	CTGTTCTTAG
3801	AGCTTGGCAT	GTAAGTTTTT	TTGAAACAGA	GTCTCGCTCT	GTCACCCAGG
3851	CTGGAGTGCA	GTGGCGCGAT	CTCGGCTCAC	TGCAACCTCT	GCCTCCCGGG
3901	TTCAGCGAT	TCTCCTGCCT	CAGTCCCCCA	AGTAGCTGGG	ACTACAGGCA
3951	CGTGCCACCA	TGCCCCGGTA	ATTTTTTTGTA	TTTTTACTAG	AGACGGGATT
4001	TCACCATGTT	AGCCAGGATG	GTCTCGATCT	CCTGACCTCG	TGATCTGCCT
4051	ACCTCAGCCT	CCCAAAGTGC	TGAGATTACA	GGCGTCAGCC	ACCGCGGCCA
4101	GCCAGCATGT	AGTTATTTAA	CCCTCACAGT	AAATAGTTAT	TCATTCCCTT
4151	TTTACAGGTG	GGGAAACTGA	AGCCCAGAGA	GGTTAAGTAA	CTCACTCCAG
4201	TGGTAGCACA	GCTCGTAAAG	GCAGTCTGCT	TTTGTGCTTT	CAGACAAAGC
4251	CATACCACAG	CCTCTCAGCC	CTGCTGGGAA	GGGTGAGGAG	GGACAGGGAG
4301	GTGGGGGGGA	AGAAGGGGTG	AGTGGAGCTG	AGGGGCTGTG	CCCTTGTTTA
4351	CACTGCATTA	GCATGGTAGC	TAAGAGGACA	AGCCCGGGAC	CCAGCACCTG
4401	GGTGTGAGCC	CTGGTTCCGC	TGCTTCCTGG	CTTTGTACCT	CGAGGCAAGG
4451	GATTTTATCT	CCTTGTGTCT	CAGCACTCTC	ATCTGTAAGA	CTGCACCACA
4501	TCAACACTCA	TCCTAAAGGG	ACTGTGAGAC	TTAAATGAAT	GAATATATGT
4551	AAGGCGCTTG	GTGAGCAGAT	AGTAAATGCA	CAATAAATCC	CCAAGTCTTC
4601	TGTTGAGTCA	GCATTTGCAA	GTGGGCCTGC	TACGGGTTAC	ACGATCATTT
4651	CCCAAGTCAC	GCCCCTGAAG	TTGCTGAGCA	GGGATAAGGG	AAGGAGTGAG
4701	CAGGCAACTC	TCTAGGCATC	ATTGAGATAA	CCCCCAACT	GAGGTACTTC
4751	TATACAGAGA	AACCCATGCC	ACTCCCAGCC	CTGCTGCCGC	CTTGAGGCCA
4801	AGACTGAGGC	TGCGGGGTGG	CCCCTCCTTG	AGTGCTTTCT	CTTCCAGGCT
4851	GGCTTTTCCG	AGCATCTGAC	CCAGACAGCA	GTCAAGTTCT	CCGCTCCACC
4901	CCGAGTTTTC	GAGAAGGGGC	ATGTAGATAG	GAGAGCCCTG	GGTCGACCTG
4951	TGTTCGAATC	CTTGCTGGGC	CTCTTGCTTT	AAATGTGTGA	CCAGAGGCAC
5001	ATGCATCCTG	TCTGAGTCTC	AGCCTCCCCA	GCCACACAGT	GGGCTTAACC
5051	TCATACCCCG	CAGGAGGCTC	GTGAGGACTG	CAAGAAGGCT	TGTGGCGGGA
5101	GCTTCCAGCA	CGTGACGGGT	ATTGCATTGG	TGTCAGCTCC	CCCAGCCTTG
5151	GGGAGGGGAC	TGGGTACCCG	CTGCAATGAA	TAAGGCTAAT	GACAGAGGGA
5201	AGGAGAGGGG	AGATGTAGAG	AGGAAGCACA	TGCATATTTT	CAGCATTAAT
5251	TTTCAGTGAC	ACAAGTAATA	CCCAAACACA	CCCTCCTGCA	AACGCTACAG
5301	ATAAAGCTAA	TGCCCTTTTG	ACCCATGTCC	CCAATCCCAG	GCTCCTGCCC
5351	CTGCCCCGGA	GTGGCCACCC	CTGGCAGTCT	GGCATGGAGC	CTTCCGGGCC
5401	TCCGTGACTA	CACCGGCATT	CGTATTTGTA	TCCCCACAAT	GGAGAGTATT
5451	TTTGTCTGTC	TCTTTTTTAT	GGCGCATATC	ATTCTGAGCA	CAGCTGTCTG
5501	ATGCTTGTTT	TTTTTTCACA	CACCAACCCG	TGCCTCATTT	TCCAACCTGG
5551	TGGAACCTCA	TTTTTTC AAC	CTCATTTTCC	TGCTGCTCAG	GAAATTCTGA
5601	AAGCCATTAA	TTCCACTGCC	AGCTCTTCTT	CCAGCTGCCA	GACGGGGCCG
5651	TCTCTGATGC	TGGCATCGC	AGTCTCGCAT	TTGAATATGT	CAAGGCCACG
5701	AGTCCTCAGG	GGCCCCGGAT	TAGCCTAACG	GGATGGGGTT	TGGCAGCCCA
5751	AGCAGGAAGA	GTTGCCAAGC	TGACGCTGCC	TCGCAAGTGC	CTTTCAGAAG
5801	AGCCCACACT	GCAGTTCCTT	CCATCACCTC	CCATCCATTC	AGGCTTCCTT
5851	GGTTAAACT	GACTGTGTGC	CAGGCCCTGG	GGAGACCAGG	ACGAGTGGGT
5901	GATGGAACCC	TTCTCTGTGC	CCGAGCTGTT	TGGAGCACAC	CTTTGATCTG
5951	GACACCATT	TGAATGTGCC	ATGTGCCATT	AAATGGGGGT	AAATGATGTG
6001	CTCTGGGGGT	GCAGAGGAAG	GTGGCAGCCA	TTCTGCCAGA	AGCTGGA ACT
6051	GGTTGCTTCT	CTTCTCAAGA	ATTTGGGCCA	ATTGCTGATT	CCTCTGGGCC
6101	TCAGTTTCT	CATCTGTGAG	ACAGGGATCT	TGTCACACCA	CAAGGCTATC
6151	AAGAGTTTGA	GCAAAAGTGG	TTGGACGCAG	TGGCTCATGC	CTGTAATCCC
6201	AGCTCTTTGG	GAGGCCGAGG	TGGGCAGATC	TCTTGAGGTC	AGGAGTTCAA
6251	GACCAGCCTG	GCTAACACAG	TGAAACACCG	TCTCTACTAA	AAAATACAAA

FIGURE 3, page 2 of 6

9451 TGGGACCCAG AACTGAGCCT GGGAGGGATC CGACAGAAAA GCTCAGGGCG
 9501 GGTCTTCTCC TTGTGCCCCG GATTGGGCTA TGCTGGGTAC CACCATGTAC
 9551 TCAGGCATGG TGGGTTTTGA ACCCATAAAC CAAAGGCCCT TGTTCATCAGC
 9601 TCTTAACAAG TATATTTTGT ATTTTAATCT CTCTAAACAT ATTGAAGTTT
 9651 TAGGGCCCTA AGGAACCTTA GTGATCTTCT ATTGGGTCTT TCTGAGGTTC
 9701 AGAGAGGGTA AGTAACTTCC TCCAGGTCAC ACAGCAAGTC TGTGGGTGGC
 9751 AGAAGCAAGC TAGCGCTGGG CATTCACTAC ATACCACGAT GTGCTCCCTC
 9801 TCTTGATGCT TGGCCCTTGG GGCCTTCAGG GCTTTGGGAC ATCTGTCTCT
 9851 CAACCTCTCT CCTAGATCAG TCTGTGAGGG TCCCTGTAGA TATTGTGTAC
 9901 ACCATGCCCA TGTATATACA AGTACACACA GATGTACACA CAGATGTACA
 9951 CATGCTCCAG CCCCAGCTCT GCATACCTGC ACCTGCACCC CAGCCTTGGC
 10001 CCCTGCCTGC GTCTGTGCTC AAAGCAGCAG CTCCAACCTT GCCTCTGTCC
 10051 CTTTCCCCAC CCACTGCCTG AGCCTTCTGA GCAGACCAGG TACCTTGGCT
 10101 GCACCGGTGT GTGGCCCGCT CTCACCCAGG CACAGCCCCG CCACCATGGA
 10151 TCTCCGTGTA CACTATCAAT AAAAGTGGGT TTGTTACAAA GCCGTGTCTT
 10201 TGCCCATGTG TATTTTTTGT ATTTCCAAGA GGAGGTGTGC CCCTTTCCAG
 10251 ACCAAAGCTG GCCTTTCCCT CCCAAAATGC ACCTGCCGTG TACCCTGGCC
 10301 CTGAGGGTCA GCACTGAGTC CACCTTCAAG TGTAAGTGTG GGGAGAGGGG
 10351 GATAAGTCCC CCAGATGGAA GGTGATGCCC TCCTTCAGCC TGGCCCTCCT
 10401 GGGTCCTCCG GGTGTGTGTA CCGAGGTGTC TGTGTCCACA AAGAAGGGGC
 10451 CCCCCTGGAC CATTAGCTCC AGGAGGATCT CCGTGTCTGA GTTCTTTGTG
 10501 ATTCCTGTAC AGCAGCAATT TCACCCGAGG GGGACAGTTG GCAATCTCTG
 10551 GAAACCTTTT CCAAGCCTGG GGCTGGGGCT GCTACTCTCA TCTGGTGGGT
 10601 GGAGGCCAGG GACACCATTG AGTATCCTCC AACGCACAGG ATGCCCTCC
 10651 ACCCCCAACC CACTGAGAAT TATCTGGCCT CAAATGCCAA GCGTGGGCAG
 10701 CTTACTTAGT ACTCACCCCA GGGGCTGGGA CACGCCCCCA CCTGCGTGTG
 10751 ATGGATTTGT TGGACCACAT TCTGGACGGA ACCCAGAGCA TAAGCACTCC
 10801 TGTGAAGTGA GACAGGATGT GGGTGAGGAT GGAAAGTGGA GGCTGAGGGA
 10851 GAAGGTCTGG GCCCTGACCA ACACGGAATG TGCCCCCTGG GACTGAGAGG
 10901 CTTCCCTGGG CAGAGGGAAA GGAGGAAGTC AGTGAGGTAA AATACTCCCT
 10951 GTGTGTTTTA CCCAGCGAGT CTCACGCCAT CCTATCACCC AGCCCCGAGG
 11001 GAAGCCCACT CATGTTCAAC CCATCTGAGC ATTTAGGCTC AGAGAGCTCA
 11051 ATATCTTGTC CAAGATGGCA CAGCTGGTGA AGTGGCAGAT CAGAGATTCA
 11101 ACACCAGAGG CTGTCTGATT TCCGTCTGGC TGAAGAAAGA TTTTGCATCA
 11151 GGGAGGTGGA AACCATCTGT GCTTTTGATC AGCAAATGCC ACCAGCAGGA
 11201 TCAGGGAGCC AGGCCATAAA G

FEATURES:

Start: 3000
 Exon: 3000-3270
 Intron: 3271-7693
 Exon: 7694-8220
 Stop: 8221

CHROMOSOME MAP POSITION:

Chromosome 22

ALLELIC VARIANTS (SNPs):

DNA

Position	Major	Minor	Domain
3951	C	T	Intron
4127	C	T	Intron
4157	G	A	Intron
4513	C	T	Intron
6894	C	A	Intron
8409	G	C	Beyond ORF (3')
8437	T	G	Beyond ORF (3')
8579	T	C	Beyond ORF (3')
10292	A	G	Beyond ORF (3')
10792	A	G	Beyond ORF (3')

Context:

DNA
Position
3951

CACACCCCAGGCCTTTGCCACCTCCTAGAGAGGTAAGGGCAGGACCCAGGCAGTGATCAC
CAAAGGGAAGGGGCTTGGTCATGGTCATAGTGATGGTGATGGCACTAGCTGACACTTAT
CAGAAGCTATGGGCTGGCCCTGTTCTTAGAGCTTGGCATGTAGTTTTTTTTTGAACAGA
GTCTCGCTCTGTACCCAGGCTGGAGTGCAGTGGCGCGATCTCGGCTCACTGCAACCTCT
GCCTCCCGGGTTCAAGCGATTCTCCTGCCTCAGTCCCCCAAGTAGCTGGGACTACAGGCA
[C, T]
GTGCCACCATGCCCGGCTAATTTTTTGTATTTTTACTAGAGACGGGATTTACCATGTTA
GCCAGGATGGTCTCGATCTCCTGACCTCGTGATCTGCCTACCTCAGCCTCCCAAAGTGCT
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AATAGTTATTTCATTCCTTTTTACAGGTGGGAAACTGAAGCCCAGAGAGGTTAAGTAAC
TCACTCCAGTGGTAGCACAGCTCGTAAAGGCAGTCTGCTTTTGTGCTTTCAGACAAAGCC

4127 CAGAGTCTCGCTCTGTACCCAGGCTGGAGTGCAGTGGCGCGATCTCGGCTCACTGCAAC
CTCTGCCTCCCGGGTTCAAGCGATTCTCCTGCCTCAGTCCCCCAAGTAGCTGGGACTACA
GGCAGTGCCACCATGCCCGGCTAATTTTTTGTATTTTTACTAGAGACGGGATTTACCA
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GTGCTGAGATTACAGGCGTCAGCCACCGCGCCAGCCAGCATGTAGTTATTTAACCTCA
[C, T]
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GGAAGAAGGGGTGAGTGGAGCTGAGGGGCTGTGCCCTTGTTTACACTGCATTAGCATGGT
AGCTAAGAGGACAAGCCCGGGACCCAGCACCTGGGTGTGAGCCCTGGTTCCGCTGCTTCC

4157 TGCAGTGGCGCGATCTCGGCTCACTGCAACCTCTGCCTCCCGGGTTCAAGCGATTCTCCT
GCCTCAGTCCCCCAAGTAGCTGGGACTACAGGCACGTGCCACCATGCCCGGCTAATTTTT
TGATTTTTTACTAGAGACGGGATTTACCATGTTAGCCAGGATGGTCTCGATCTCCTGAC
CTCGTGATCTGCCTACCTCAGCCTCCCAAAGTGCTGAGATTACAGGCGTCAGCCACCGCG
GCCAGCCAGCATGTAGTTATTTAACCTCACAGTAAATAGTTATTTCATTCCTTTTTTACA
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GAAGGGTGAGGAGGGACAGGGAGGTTGGGGGGAAGAAGGGGTGAGTGGAGCTGAGGGGCT
GTGCCCTTGTTTACACTGCATTAGCATGGTAGCTAAGAGGACAAGCCCGGGACCCAGCAC
CTGGGTGTGAGCCCTGGTTCCGCTGCTTCTGGCTTTGTACCTCGAGGCAAGGGATTTTA

4513 TCGTAAAGGCAGTCTGCTTTTGTGCTTTTACAGACAAAGCCATACCACAGCCTCTCAGCCCT
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GGGCTGTGCCC'TGT'TTACACTGCATTAGCATGGTAGCTAAGAGGACAAGCCCGGACCC
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[C, T]
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6894 GCACTCCAGCCTGGGCCACAGAGAAAGACTCCATCTCAAAAAAAAAAAAAAAAAAAAAA
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AGTCCAGACAGCCTCCCCACCACCCACCGTCTCCACAGCAGCCCTGTTTCAGATTAC
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8409 CATGGTCTCGCCCTTCGCCCGCCGCCAGCGTCAACAGTGACCTCAAGTACATCAAGGC
CAAGGTCTTCGGGAAGGCCAGGCCCGTGAGAGGGACAAGTGACCATCCAGTGAGCGAG
GGATGCTGGGGCGGGGCTTGGCCAGTGCCTTCAGGGAGGTGGCCCCAGATGCCCACTGTG
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[G, C]
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AAAGGACACAGAAGGCCAGATGAGAAAGGTCTCCTCTCTCCTGGCATAACACCCAGCTTG
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8437 AGCGTCAACAGTGACCTCAAGTACATCAAGGCCAAGGTCTTCGGGAAGGCCAGGCCCGT
GAGAGGGACAAGTGACCATCCAGTGAGCGAGGGATGCTGGGGCGGGGCTTGGCCAGTGC
CTTCAGGGAGGTGGCCCCAGATGCCCACTGTGCGCATCTCCCCACCGAGGCCCGCGCAGC
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[T, G]
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8579 GCCCACTGTGCGCATCTCCCCACCGAGGCCCGCGCAGCAGTCTTGTTACAGACCTTAGG
CACCAGACTGGAGGCCCGGGCGCTGGCCTCCGCACATTTCGTCTGCCTTCTCACAGCTT
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[T, C]
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TAGACCACGCCCACCACTTAGACCACGCCCACCTCCTGACCGCTTCTCAGCCTCCTCT

10292 AGCCTTGGCCCCCTGCCTGCGTCTGTGCTCAAAGCAGCAGCTCCAACCTGCCTCTGTCCC
CTTCCCCACCACTGCCTGAGCCTTCTGAGCAGACCAGGTACCTTGGCTGCACCGTGTG
TGCCCCGCTCTCACCCAGGCACAGCCCCGCCACCATGGATCTCCGTGTACACTATCAATA
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GAGGTGTGCCCTTTCAGACCAAAGCTGGCCTTCCCTCCCAAATGCACCTGCCGTGT
[A, G]
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GACAGTTGGCAATCTCTGGAACCTTTTCAAGCCTGGGGCTGGGGCTGCTACTCTCATC

10792 TTCTTTGTGATTCTGTACAGCAGCAATTTACCCGCAGGGGACAGTTGGCAATCTCTGG
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ATCTGGCCTCAAATGCCAAGCGTGGGCAGCCTTACTTAGACTCACCCAGGGGCTGGGAC
ACGCCCCACCTGCGTGTGATGGATTTGTTGGACCACATTCTGGACGGAACCCACAGCAT
[A, G]
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CACGCCATCCTATACCCAGCCCCAGGGAAGCCCACTCATGTTACCCCATCTGAGCAT
TTAGGCTCAGAGAGCTCAATATCTTGTCCAAGATGGCACAGCTGGTGAAGTGGCAGATCA